We claim:

1. A process for preparing zeaxanthin and/or biosynthetic intermediates and/or secondary products thereof by culturing genetically modified plants which, compared to the wild type, have a reduced ε-cyclase activity caused by double-stranded ε-cyclase ribonucleic acid sequences.

2. The process according to claim 1, wherein an RNA is introduced into the plant, which has a double-stranded structural region and comprises, in said region, a nucleic acid sequence which

   a) is identical to at least part of the ε-cyclase transcript intrinsic to said plant and/or

   b) is identical to at least part of the ε-cyclase-promoter sequence intrinsic to said plant.

3. The process according to claim 2, wherein the double-stranded structural region comprises a nucleic acid sequence which is identical to at least part of the ε-cyclase transcript intrinsic to the plant and which comprises the 5′ end or the 3′ end of the nucleic acids coding for a ε-cyclase and intrinsic to the plant.

4. The process according to either of claims 2 and 3, wherein the double-stranded structural region comprises in each case a sense-RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least part of the sense-RNA ε-cyclase transcript, and comprises an antisense-RNA strand which is essentially complementary to the sense-RNA strand.

5. The process according to any of claims 1 to 4, wherein genetically modified plants are used whose flowers have the lowest rate of expression of an ε-cyclase.

6. The process according to claim 5, wherein the double-stranded ε-cyclase ribonucleic acid sequence is transcribed under the control of a flower-specific promoter.

Sequences + drawings.

7. The process according to any of claims 1 to 6, wherein the plant used is a plant selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassicaceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae.

8. The process according to claim 7, wherein the plant used is a plant selected from the plant genera Marigold, Tagetes, Acacia, Aconitum, Adonis, Arnica, Aquilegia, Aster, Astragalus, Bignonia, Calendula, Caltha, Campanula, Canna, Centaurea, Cheiranthus, Chrysanthemum, Citrus, Crepis, Crocus, Curcurbita, Cytisus, Delonia, Delphinium, Dianthus, Dimorphotheca, Doronicum, Eschscholtzia, Forsythia, Fremontia, Gazania, Gelsemium, Genista, Gentiana, Geranium, Gerbera, Geum, Grevilla, Helenium, Helianthus, Hepatica, Heracleum, Hibiscus, Heliopsis, Hypericum, Hypochoeris, Impatiens, Iris, Jacaranda, Kerria, Laburnum, Lathyrus, Leontodon, Lilium, Linum, Lotus, Lycopersicon, Lysimachia, Maratia, Medicago, Mimulus, Narcissus, Oenothera, Osmanthus, Petunia, Photinia, Physalis, Phyteuma, Potentilla, Pyracantha, Ranunculus, Rhododendron, Rosa, Rudbeckia, Senecio, Silene, Silphium, Sinapsis, Sorbus, Spartium, Tecoma, Torenia, Tragopogon, Trollius, Tropaeolum, Tulipa, Tussilago, Ulex, Viola or Zinnia.

9. The process according to claim 8, wherein the plant used is a plant selected from the plant species Marigold, Tagetes erecta or Tagetes patula.

10. The process according to any of claims 1 to 9, wherein the genetically modified plants are harvested after cultivation and subsequently zeaxanthin and/or its biosynthetic intermediates and/or secondary products are isolated from said plants.

11. The process according to any of claims 1 to 10, wherein the biosynthetic intermediates and/or secondary products are selected from the group consisting of lycopene, β-carotene, astaxanthin, canthaxanthin, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, adonirubin adonixanthin,

antheraxanthin, violaxanthin, neoxanthin, capsorubin, and capsanthin.

12. A ribonucleic acid construct, comprising RNA which has a double-stranded structural region and comprises, in said region, a nucleic acid sequence which

a) is identical to at least part of the ε-cyclase transcript intrinsic to said plant and/or

b) is identical to at least part of the ε-cyclase-promoter sequence intrinsic to said plant.

13. A nucleic acid construct, transcribable into

a) a sense-RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least part of the sense-RNA ε-cyclase transcript, and

b) an antisense-RNA strand which is essentially, preferably fully, complementary to the RNA sense strand under a).

14. A nucleic acid construct, comprising

a) a sense-DNA strand which is essentially identical to at least part of the promoter region of an ε-cyclase gene, and

b) an antisense-DNA strand which is essentially, preferably fully, complementary to the DNA sense strand under a).

15. The nucleic acid construct according to claim 13, wherein SEQ ID No. 4 describes the cDNA sequence deducible from the ε-cyclase transcript.

16. The nucleic acid construct according to claim 14, wherein SEQ ID No. 13 describes the nucleic acid sequence of the promoter region of the ε-cyclase gene.

17. The nucleic acid construct according to any of claims 12 to 16, wherein the sense-RNA and antisense-RNA strands are covalently connected to one another in the form of an inverted repeat.

18. The nucleic acid construct according to any of claims 12 to 17, wherein the nucleic acid construct additionally comprises a promoter in a functionally linked manner.

19. The nucleic acid construct according to claim 18, wherein a flower-specific promoter is used.

20. A process for preparing genetically modified plants, wherein expression cassettes comprising a nucleic acid construct according to any of claims 12 to 19 are introduced into a parent plant.

21. A genetically modified plant which, compared to the wild type, has a reduced ε-cyclase activity caused by double-stranded ε-cyclase ribonucleic acid sequences.

22. The genetically modified plant according to claim 21, wherein said genetically modified plant comprises an RNA which has a double-stranded structural region and comprises, in said region, a nucleic acid sequence which,

a) is identical to at least part of the ε-cyclase transcript intrinsic to said plant and/or

b) is identical to at least part of the ε-cyclase-promoter sequence intrinsic to said plant.

23. The genetically modified plant according to claim 21 or 22, wherein the plant is selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassicaceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae.

24. The genetically modified plant according to claim 23, wherein the plant is selected from the plant genera Marigold, Tagetes, Acacia, Aconitum, Adonis, Arnica, Aquilegia, Aster, Astragalus, Bignonia, Calendula, Caltha, Campanula, Canna, Centaurea, Cheiranthus, Chrysanthemum, Citrus, Crepis, Crocus, Curcurbita, Cytisus, Delonia, Delphinium, Dianthus, Dimorphoteca, Doronicum, Escholtzia, Forsythia, Fremontia, Gazania, Gelsemium, Genista, Gentiana, Geranium, Gerbera,

Geum, Grevilla, Helenium, Helianthus, Hepatica, Heracleum, Hisbiscus, Heliopsis, Hyperricum, Hypochoeris, Impatiens, Iris, Jacaranda, Kerria, Laburnum, Lathyrus, Leontodon, Lilium, Linum, Lotus, Lycopersicon, Lysimachia, Maratia, Medicago, Mimulus, Narcissus, Oenothera, Osmanthus, Petunia, Photinia, Physalis, Phyteuma, Potentilla, Pyracantha, Ranunculus, Rhododendron, Rosa, Rudbeckia, Senecio, Silene, Silphium, Sinapsis, Sorbus, Spartium, Tecoma, Torenia, Tragopogon, Trollius, Tropaeolum, Tulipa, Tussilago, Ulex, Viola or Zinnia.

25. The genetically modified plant according to claim 24, wherein the plant is selected from the plant species Marigold, Tagetes erecta or Tagetes patula.

26. The use of the genetically modified plants according to any of claims 21 to 25 as ornamental plants or as feedstuffs and foodstuffs.

27. The use of the genetically modified plants according to any of claims 21 to 25 for preparing carotenoid-containing extracts or for preparing feed and food supplements.